SEQUENCE LISTING

<110> Ecole Polytechnique Fédérale de Lausanne (EPFL)

<120> Method for identification of suitable fragmentation sites in a reporter
protein

<130> PEPF001WO

<150> US 34,404 JM-213
<151> 2003-10-09

<160> 66

<170> PatentIn version 3.1

<210> 1
<211> 672
<212> DNA
<213> Saccharomyces cerevisiae

<220>
<221> modified_base
<222> (186)..(186)
<223> silent point mutation introduced to generate HindIII restriction
       site

<300>
<308> NCBI / NC_001136
<309> 2004-08-30

<400> 1
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agcacagagg ccgcagaatg tgctctagat tccgatgctg acttgctggg tattatatgt   120

gtgcccaata gaaagagaac aattgacccg gttattgcaa ggaaaatttc aagtcttgta   180

aaagcatata aaaatagttc aggcactccg aaatacttgg ttggcgtgtt cgtaatcaa   240

cctaaggagg atgttttggc tctggtcaat gattacggca ttgatatcgt ccaactgcac   300

ggagatgagt cgtggcaaga ataccaagag ttcctcggtt tgccagttat taaaagactc   360

gtatttccaa aagactgcaa catactactc agtgcagctt cacagaaacc tcattcgttt   420

attcccttgt ttgattcaga agcaggtggg acaggtgaac ttttggattg gaactcgatt   480

tctgactggg ttggaaggca agagagcccc gagagcttac attttatgtt agctggtgga   540

ctgacgccag aaaatgttgg tgatgcgctt agattaaatg gcgttattgg tgttgatgta   600

agcggaggtg tggagacaaa tggtgtaaaa gactctaaca aaatagcaaa tttcgtcaaa   660

aatgctaaga aa   672

<210> 2
<211> 224
<212> PRT
<213> Saccharomyces cerevisiae

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<300>
<308>  NCBI / NC_001136
<309>  2004-08-30

<400>  2

Met Ser Val Ile Asn Phe Thr Gly Ser Ser Gly Pro Leu Val Lys Val
1               5                   10                  15


Cys Gly Leu Gln Ser Thr Glu Ala Ala Glu Cys Ala Leu Asp Ser Asp
                20                  25                  30


Ala Asp Leu Leu Gly Ile Ile Cys Val Pro Asn Arg Lys Arg Thr Ile
        35                  40                  45


Asp Pro Val Ile Ala Arg Lys Ile Ser Ser Leu Val Lys Ala Tyr Lys
        50                  55                  60


Asn Ser Ser Gly Thr Pro Lys Tyr Leu Val Gly Val Phe Arg Asn Gln
65                  70                  75                  80


Pro Lys Glu Asp Val Leu Ala Leu Val Asn Asp Tyr Gly Ile Asp Ile
                85                  90                  95


Val Gln Leu His Gly Asp Glu Ser Trp Gln Glu Tyr Gln Glu Phe Leu
                100                 105                 110


Gly Leu Pro Val Ile Lys Arg Leu Val Phe Pro Lys Asp Cys Asn Ile
                115                 120                 125


Leu Leu Ser Ala Ala Ser Gln Lys Pro His Ser Phe Ile Pro Leu Phe
        130                 135                 140


Asp Ser Glu Ala Gly Gly Thr Gly Glu Leu Leu Asp Trp Asn Ser Ile
145                 150                 155                 160


Ser Asp Trp Val Gly Arg Gln Glu Ser Pro Glu Ser Leu His Phe Met
                165                 170                 175


Leu Ala Gly Gly Leu Thr Pro Glu Asn Val Gly Asp Ala Leu Arg Leu
                180                 185                 190


Asn Gly Val Ile Gly Val Asp Val Ser Gly Gly Val Glu Thr Asn Gly
                195                 200                 205


Val Lys Asp Ser Asn Lys Ile Ala Asn Phe Val Lys Asn Ala Lys Lys
210                 215                 220


<210>  3
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<211>   132
<212>   DNA
<213>   Saccharomyces cerevisiae

<220>
<221>   modified_base
<222>   (22)..(22)
<223>   point mutation


<400>   3
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agcacagagg ccgcagaatg tgctctagat tccgatgctg acttgctggg tattatatgt       120

gtgcccaata ga                                                           132


<210>   4
<211>   44
<212>   PRT
<213>   Saccharomyces cerevisiae

<400>   4

Met Ser Val Ile Asn Phe Thr Cys Ser Ser Gly Pro Leu Val Lys Val
1               5                  10                  15


Cys Gly Leu Gln Ser Thr Glu Ala Ala Glu Cys Ala Leu Asp Ser Asp
            20                  25                  30


Ala Asp Leu Leu Gly Ile Ile Cys Val Pro Asn Arg
            35                  40


<210>   5
<211>   540
<212>   DNA
<213>   Saccharomyces cerevisiae

<400>   5
aagagaacaa ttgacccggt tattgcaagg aaaatttcaa gtcttgtaaa agcatataaa        60

aatagttcag gcactccgaa atacttggtt ggcgtgtttc gtaatcaacc taaggaggat       120

gttttggctc tggtcaatga ttacggcatt gatatcgtcc aactgcacgg agatgagtcg       180

tggcaagaat accaagagtt cctcggtttg ccagttatta aaagactcgt atttccaaaa       240

gactgcaaca tactactcag tgcagcttca cagaaacctc attcgtttat tcccttgttt       300

gattcagaag caggtgggac aggtgaactt ttggattgga actcgatttc tgactgggtt       360

ggaaggcaag agagccccga gagcttacat tttatgttag ctggtggact gacgccagaa       420

aatgttggtg atgcgcttag attaaatggc gttattggtg ttgatgtaag cggaggtgtg       480

gagacaaatg gtgtaaaaga ctctaacaaa atagcaaatt tcgtcaaaaa tgctaagaaa       540


<210>   6
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<211> 180
<212> PRT
<213> Saccharomyces cerevisiae

<400> 6

Lys Arg Thr Ile Asp Pro Val Ile Ala Arg Lys Ile Ser Ser Leu Val
1   5   10   15

Lys Ala Tyr Lys Asn Ser Ser Gly Thr Pro Lys Tyr Leu Val Gly Val
            20   25   30

Phe Arg Asn Gln Pro Lys Glu Asp Val Leu Ala Leu Val Asn Asp Tyr
        35   40   45

Gly Ile Asp Ile Val Gln Leu His Gly Asp Glu Ser Trp Gln Glu Tyr
    50   55   60

Gln Glu Phe Leu Gly Leu Pro Val Ile Lys Arg Leu Val Phe Pro Lys
65   70   75   80

Asp Cys Asn Ile Leu Leu Ser Ala Ala Ser Gln Lys Pro His Ser Phe
            85   90   95

Ile Pro Leu Phe Asp Ser Glu Ala Gly Gly Thr Gly Glu Leu Leu Asp
            100   105   110

Trp Asn Ser Ile Ser Asp Trp Val Gly Arg Gln Glu Ser Pro Glu Ser
            115   120   125

Leu His Phe Met Leu Ala Gly Gly Leu Thr Pro Glu Asn Val Gly Asp
    130   135   140

Ala Leu Arg Leu Asn Gly Val Ile Gly Val Asp Val Ser Gly Gly Val
145   150   155   160

Glu Thr Asn Gly Val Lys Asp Ser Asn Lys Ile Ala Asn Phe Val Lys
                165   170   175

Asn Ala Lys Lys
            180

<210> 7
<211> 159
<212> DNA
<213> Saccharomyces cerevisiae

<400> 7
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agcacagagg ccgcagaatg tgctctagat tccgatgctg acttgctggg tattatatgt   120

gtgcccaata gaaagagaac aattgacccg gttattgca   159

<210>   8
<211>   53
<212>   PRT
<213>   Saccharomyces cerevisiae

<400>   8

Met Ser Val Ile Asn Phe Thr Gly Ser Ser Gly Pro Leu Val Lys Val
1   5   10   15

Cys Gly Leu Gln Ser Thr Glu Ala Ala Glu Cys Ala Leu Asp Ser Asp
            20   25   30

Ala Asp Leu Leu Gly Ile Ile Cys Val Pro Asn Arg Lys Arg Thr Ile
        35   40   45

Asp Pro Val Ile Ala
     50

<210>   9
<211>   516
<212>   DNA
<213>   Saccharomyces cerevisiae

<400>   9
gcaaggaaaa tttcaagtct tgtaaaagct tataaaaata gttcaggcac tccgaaatac   60

ttggttggcg tgtttcgtaa tcaacctaag gaggatgttt tggctctggt caatgattac   120

ggcattgata tcgtccaact gcacggagat gagtcgtggc aagaatacca agagttcctc   180

ggtttgccag ttattaaaag actcgtattt ccaaaagact gcaacatact actcagtgca   240

gcttcacaga aacctcattc gtttattccc ttgtttgatt cagaagcagg tgggacaggt   300

gaactttgg attggaactc gatttctgac tgggttggaa ggcaagagag ccccgagagc   360

ttacatttta tgttagctgg tggactgacg ccagaaaatg ttggtgatgc gcttagatta   420

aatggcgtta ttggtgttga tgtaagcgga ggtgtggaga caaatggtgt aaaagactct   480

aacaaaatag caaatttcgt caaaaatgct aagaaa   516

<210>   10
<211>   172
<212>   PRT
<213>   Saccharomyces cerevisiae

<400>   10

Ala Arg Lys Ile Ser Ser Leu Val Lys Ala Tyr Lys Asn Ser Ser Gly
1   5   10   15

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Thr Pro Lys Tyr Leu Val Gly Val Phe Arg Asn Gln Pro Lys Glu Asp
        20              25              30

Val Leu Ala Leu Val Asn Asp Tyr Gly Ile Asp Ile Val Gln Leu His
        35              40              45

Gly Asp Glu Ser Trp Gln Glu Tyr Gln Glu Phe Leu Gly Leu Pro Val
    50              55              60

Ile Lys Arg Leu Val Phe Pro Lys Asp Cys Asn Ile Leu Leu Ser Ala
65              70              75              80

Ala Ser Gln Lys Pro His Ser Phe Ile Pro Leu Phe Asp Ser Glu Ala
            85              90              95

Gly Gly Thr Gly Glu Leu Leu Asp Trp Asn Ser Ile Ser Asp Trp Val
            100             105             110

Gly Arg Gln Glu Ser Pro Glu Ser Leu His Phe Met Leu Ala Gly Gly
        115             120             125

Leu Thr Pro Glu Asn Val Gly Asp Ala Leu Arg Leu Asn Gly Val Ile
    130             135             140

Gly Val Asp Val Ser Gly Gly Val Glu Thr Asn Gly Val Lys Asp Ser
145             150             155             160

Asn Lys Ile Ala Asn Phe Val Lys Asn Ala Lys Lys
            165             170
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<210> 11
<211> 561
<212> DNA
<213> Saccharomyces cerevisiae

<400> 11

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agcacagagg ccgcagaatg tgctctagat tccgatgctg acttgctggg tattatatgt     120

gtgcccaata gaaagagaac aattgacccg gttattgcaa ggaaaatttc aagtcttgta     180

aaagcttata aaaatagttc aggcactccg aaatacttgg ttggcgtgtt cgtaatcaa      240

cctaaggagg atgttttggc tctggtcaat gattacggca ttgatatcgt ccaactgcac     300

ggagatgagt cgtggcaaga ataccaagag ttcctcggtt tgccagttat taaaagactc     360

gtatttccaa aagactgcaa catactactc agtgcagctt cacagaaacc tcattcgttt     420

attcccttgt ttgattcaga agcaggtggg acaggtgaac ttttggattg gaactcgatt     480

tctgactggg ttggaaggca agagagcccc gagagcttac attttatgtt agctggtgga     540
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ctgacgccag aaaatgttgg t   561

<210> 12
<211> 187
<212> PRT
<213> Saccharomyces cerevisiae

<400> 12

Met Ser Val Ile Asn Phe Thr Gly Ser Ser Gly Pro Leu Val Lys Val
1   5   10   15

Cys Gly Leu Gln Ser Thr Glu Ala Ala Glu Cys Ala Leu Asp Ser Asp
            20   25   30

Ala Asp Leu Leu Gly Ile Ile Cys Val Pro Asn Arg Lys Arg Thr Ile
        35   40   45

Asp Pro Val Ile Ala Arg Lys Ile Ser Ser Leu Val Lys Ala Tyr Lys
    50   55   60

Asn Ser Ser Gly Thr Pro Lys Tyr Leu Val Gly Val Phe Arg Asn Gln
65   70   75   80

Pro Lys Glu Asp Val Leu Ala Leu Val Asn Asp Tyr Gly Ile Asp Ile
            85   90   95

Val Gln Leu His Gly Asp Glu Ser Trp Gln Glu Tyr Gln Glu Phe Leu
            100   105   110

Gly Leu Pro Val Ile Lys Arg Leu Val Phe Pro Lys Asp Cys Asn Ile
        115   120   125

Leu Leu Ser Ala Ala Ser Gln Lys Pro His Ser Phe Ile Pro Leu Phe
    130   135   140

Asp Ser Glu Ala Gly Gly Thr Gly Glu Leu Leu Asp Trp Asn Ser Ile
145   150   155   160

Ser Asp Trp Val Gly Arg Gln Glu Ser Pro Glu Ser Leu His Phe Met
            165   170   175

Leu Ala Gly Gly Leu Thr Pro Glu Asn Val Gly
            180   185

<210> 13
<211> 111
<212> DNA
<213> Saccharomyces cerevisiae

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<400>  13
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ggtgtaaaag actctaacaa aatagcaaat ttcgtcaaaa atgctaagaa a              111


<210>  14
<211>  37
<212>  PRT
<213>  Saccharomyces cerevisiae

<400>  14

Asp Ala Leu Arg Leu Asn Gly Val Ile Gly Val Asp Val Ser Gly Gly
1               5                  10                  15


Val Glu Thr Asn Gly Val Lys Asp Ser Asn Lys Ile Ala Asn Phe Val
            20                  25                  30


Lys Asn Ala Lys Lys
            35



<210>  15
<211>  612
<212>  DNA
<213>  Saccharomyces cerevisiae

<220>
<221>  mutation
<222>  (22)..(22)
<223>  point mutation


<220>
<221>  deletion
<222>  (612)..(612)
<223>  missing sequence after base 612 of wild-type: GAGACAAATGGTGTAAAAG
       ACTCT


<400>  15
atgtctgtta ttaatttcac atgtagttct ggtccattgg tgaaagtttg cggcttgcag      60

agcacagagg ccgcagaatg tgctctagat tccgatgctg acttgctggg tattatatgt     120

gtgcccaata gaaagagaac aattgacccg gttattgcaa ggaaaatttc aagtcttgta     180

aaagcttata aaaatagttc aggcactccg aaatacttgg ttggcgtgtt tcgtaatcaa     240

cctaaggagg atgttttggc tctggtcaat gattacggca ttgatatcgt ccaactgcac     300

ggagatgagt cgtggcaaga ataccaagag ttcctcggtt tgccagttat taaaagactc     360

gtatttccaa aagactgcaa catactactc agtgcagctt cacagaaacc tcattcgttt     420

attcccttgt ttgattcaga agcaggtggg acaggtgaac ttttggattg gaactcgatt     480

tctgactggg ttggaaggca agagagcccc gagagcttac attttatgtt agctggtgga     540
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ctgacgccag aaaatgttgg tgatgcgctt agattaaatg gcgttattgg tgttgatgta   600

agcggaggtg tg   612

<210> 16
<211> 204
<212> PRT
<213> Saccharomyces cerevisiae

<400> 16

Met Ser Val Ile Asn Phe Thr Cys Ser Ser Gly Pro Leu Val Lys Val
1   5   10   15

Cys Gly Leu Gln Ser Thr Glu Ala Ala Glu Cys Ala Leu Asp Ser Asp
                20   25   30

Ala Asp Leu Leu Gly Ile Ile Cys Val Pro Asn Arg Lys Arg Thr Ile
            35   40   45

Asp Pro Val Ile Ala Arg Lys Ile Ser Ser Leu Val Lys Ala Tyr Lys
    50   55   60

Asn Ser Ser Gly Thr Pro Lys Tyr Leu Val Gly Val Phe Arg Asn Gln
65   70   75   80

Pro Lys Glu Asp Val Leu Ala Leu Val Asn Asp Tyr Gly Ile Asp Ile
                85   90   95

Val Gln Leu His Gly Asp Glu Ser Trp Gln Glu Tyr Gln Glu Phe Leu
            100   105   110

Gly Leu Pro Val Ile Lys Arg Leu Val Phe Pro Lys Asp Cys Asn Ile
            115   120   125

Leu Leu Ser Ala Ala Ser Gln Lys Pro His Ser Phe Ile Pro Leu Phe
    130   135   140

Asp Ser Glu Ala Gly Gly Thr Gly Glu Leu Leu Asp Trp Asn Ser Ile
145   150   155   160

Ser Asp Trp Val Gly Arg Gln Glu Ser Pro Glu Ser Leu His Phe Met
                165   170   175

Leu Ala Gly Gly Leu Thr Pro Glu Asn Val Gly Asp Ala Leu Arg Leu
            180   185   190

Asn Gly Val Ile Gly Val Asp Val Ser Gly Gly Val
            195   200

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<210>  17
<211>  36
<212>  DNA
<213>  Saccharomyces cerevisiae

<220>
<221>  mutation
<222>  (1)..(1)
<223>  missing sequence before base 1 of SEQ17, corresponding to base 63
       7 of wild-type: GAGACAAATGGTGTAAAAGACTCT


<400>  17
aacaaaatag caaatttcgt caaaaatgct aagaaa                              36


<210>  18
<211>  12
<212>  PRT
<213>  Saccharomyces cerevisiae

<400>  18

Asn Lys Ile Ala Asn Phe Val Lys Asn Ala Lys Lys
1               5                   10


<210>  19
<211>  43
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  first of a pair of peptides (together with peptide C2), that asso
       ciate into an anti-parallel coiled coil (Biochemistry 37 (1998),
       12603-12610)

<400>  19

Met Asp Tyr Lys Asp Glu Ser Gly Gln Ala Leu Glu Lys Glu Leu Ala
1               5                   10                  15


Gln Asn Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu Leu Ala Gln Leu
            20                  25                  30


Glu Lys Glu Leu Gln Ala Gly Ser Gly Ser Gly
            35                  40


<210>  20
<211>  50
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  second of a pair of peptides (together with peptide C1), that ass
       ociate into an anti-parallel coiled coil (Biochemistry 37 (1998),
       12603-12610)

<400>  20
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Gly Gly Ser Gly Ser Gly Gln Ala Leu Lys Lys Lys Leu Ala Gln Leu
1               5               10              15

Lys Trp Lys Leu Gln Ala Leu Lys Lys Lys Asn Ala Gln Leu Lys Lys
            20              25              30

Lys Leu Gln Ala Gly Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ala
        35              40              45

Phe Leu
    50
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<210>  21
<211>  39
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Primer for Ctrp fusions

<400>  21
cgatacgaat tcatggacaa ggattgtgaa atgaaacgc                         39


<210>  22
<211>  45
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Primer for pRS316-C1/2CUP1

<400>  22
aaaggaattg gcccaaaatg agtgggagtt acaagcactt gagaa                  45


<210>  23
<211>  45
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Primer for pRS316-C1/2CUP1

<400>  23
ctcaatgttc gtgaactctt cctcgagcga gttgaactct tcctc                  45


<210>  24
<211>  45
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Primer for pRS316-C1/2CUP1

<400>  24
ctccttctca agttgagcga gctccttctc aagtgcttgt aactc                  45
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<210> 25
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer for pRS316-C1/2CUP1

<400> 25
ggcacttaag aagaagttgg cgcagcttaa gtggaaactg ca   42

<210> 26
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer for pRS316-C1/2CUP1

<400> 26
agctgggcat tcttcttctt aagagcttgc agtttccact taagct   46

<210> 27
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer for pRS316-C1/2CUP1

<400> 27
aagaagaaga atgcccagct taagaagaag ctccaggctg gaagttac   48

<210> 28
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer for pRS316-C1/2CUP1

<400> 28
atacgatgtt ccagattacg ctgcattttt ataagtcgac tggtc   45

<210> 29
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer for pRS316-C1/2CUP1

<400> 29
gaccagtcga cttataaaaa tg   22

<210> 30

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<211>  25
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Primer for circular permutation of TRP1

<400>  30
gtaaaagctt ataaaaatag ttcag                                        25


<210>  31
<211>  36
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Primer for circular permutation of TRP1

<400>  31
gaaatagcct aggatgtctg ttattaattt cacagg                            36


<210>  32
<211>  35
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Primer for circular permutation of TRP1

<400>  32
cagacatcct aggctatttc ttagcatttt tgacg                             35


<210>  33
<211>  25
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Primer for circular permutation of TRP1

<400>  33
tttataagct tttacaagac ttgaa                                        25


<210>  34
<211>  22
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Primer for pRS316-C1/2CUP1

<400>  34
gtaacgaatt catggactac aa                                           22


<210>  35
<211>  66
<212>  DNA
<213>  Artificial Sequence
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<220>
<223>  Primer for pRS316-C1/2CUP1

<400>  35
cattttgggc caattccttt tccagtgctt gaccactttc gtctttgtag tccatgaatt        60

cgttac                                                                    66


<210>  36
<211>  64
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Primer for pRS316-C1/2CUP1

<400>  36
caacttcttc ttaagtgcct gacctgatcc agatccaccg ttaacacctg aacctgatcc        60

ggcc                                                                      64


<210>  37
<211>  43
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Primer for pRS316-C1/2CUP1

<400>  37
gtaatctgga acatcgtatg ggtaacttcc agcctggagc ttc                          43


<210>  38
<211>  66
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Primer for homologous recombination

<400>  38
gactctaaca aaatagcaaa tttcgtcaaa aatgctaaga aatagagggc cgcatcatgt        60

aattag                                                                    66


<210>  39
<211>  65
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Primer for homologous recombination

<400>  39
aactttcacc aatggaccag aactacctgt gaattaata acagacattt tgagatccgg        60

gtttt                                                                     65
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<210>  40
<211>  40
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Primer for Ctrp fusions

<400>  40
gcctgatcca gatccgcctt ctggtgattc atcatcttca                    40


<210>  41
<211>  40
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Primer for Ctrp fusions

<400>  41
ggcggatctg gatcaggcaa gagaacaatt gacccggtta                    40


<210>  42
<211>  40
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Primer for Ctrp fusions

<400>  42
gcctgatcca gatccgccta taaaaggtat tccgacacca                    40


<210>  43
<211>  39
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Primer for Ntrp fusions

<400>  43
gcctgatcca gatccgcctg caataaccgg gtcaattgt                     39


<210>  44
<211>  40
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Primer for Ctrp fusions

<400>  44
ggcggatctg gatcaggcgc aaggaaaatt tcaagtcttg                    40


<210>  45
<211>  42
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<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Primer for Ntrp fusions

<400>  45
gcctgatcca gatccgccac caacatttttc tggcgtcagt cc                              42


<210>  46
<211>  39
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Primer for Ctrp fusions

<400>  46
ggcggatctg gatcaggcga tgcgcttaga ttaaatggc                                  39


<210>  47
<211>  39
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Primer for Ntrp fusions

<400>  47
gcctgatcca gatccgccca cacctccgct tacatcaac                                  39


<210>  48
<211>  28
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Primer for Ctrp fusions

<400>  48
ggcggatctg gatcaggcaa caaaatag                                              28


<210>  49
<211>  25
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Primer for pRS315CUP1/ pRS316CUP1

<400>  49
agcaggatcc cattaccgac atttg                                                 25


<210>  50
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<212>  DNA
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<220>
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